#2

RAW SEQUENCE LISTING   DATE: 01/16/2002
PATENT APPLICATION: US/09/903,068   TIME: 15:53:53

Input Set : N:\Crf3\RULE60\09903068.raw
Output Set: N:\CRF3\01162002\I903068.raw

SEQUENCE LISTING

```
  3  (1) GENERAL INFORMATION:
  5       (i) APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
  6                      Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
  8      (ii) TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
  9                               Having Serine Threonine Kinase Domains And Their Use
 11     (iii) NUMBER OF SEQUENCES: 29
 13      (iv) CORRESPONDENCE ADDRESS:
 14           (A) ADDRESSEE: Felfe & Lynch
 15           (B) STREET: 805 Third Avenue
 16           (C) CITY: New York City
 17           (D) STATE: New York
 18           (F) ZIP: 10022
 20       (v) COMPUTER READABLE FORM:
 21           (A) MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 22           (B) COMPUTER: IBM
 23           (C) OPERATING SYSTEM: PC-DOS
 24           (D) SOFTWARE: Wordperfect
 26      (vi) CURRENT APPLICATION DATA:
C--> 27       (A) APPLICATION NUMBER: US/09/903,068
C--> 28       (B) FILING DATE: 11-Jul-2001
 62     (vii) PRIOR APPLICATION DATA:
 31           (A) APPLICATION NUMBER: 09/679,187
 32           (B) FILING DATE:
 35           (A) APPLICATION NUMBER: PCT/GB93/02367
 36           (B) FILING DATE: 17-November-1993
 39           (A) APPLICATION NUMBER: 9224057.1
 40           (B) FILING DATE: 17-November-1992
 43           (A) APPLICATION NUMBER: 9304677.9
 44           (B) FILING DATE: 8-March-1993
 47           (A) APPLICATION NUMBER: 9304680.3
 48           (B) FILING DATE: 8-March-1993
 51           (A) APPLICATION NUMBER: 9311047.6
 52           (B) FILING DATE: 28-May-1993
 55           (A) APPLICATION NUMBER: 9313763.6
 56           (B) FILING DATE: 2-July-1993
 59           (A) APPLICATION NUMBER: 9136099.2
 60           (B) FILING DATE: 3-August-1993
 63           (A) APPLICATION NUMBER: 9321344.5
 64           (B) FILING DATE: 15-October-1993
 66    (viii) ATTORNEY/AGENT INFORMATION:
 67           (A) NAME: Kohlei, Vineet
 68           (B) REGISTRATION NUMBER: 37,003
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ENTERED

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69              (C) REFERENCE/DOCKET NUMBER: LUD 5298
71      (ix) TELECOMMUNICATION INFORMATION:
72              (A) TELEPHONE: (212) 688-9200
73              (B) TELEFAX: (212) 838-3884
77 (2) INFORMATION FOR SEQ ID NO: 1:
78       (i) SEQUENCE CHARACTERISTICS:
79              (A) LENGTH: 1984 base pairs
80              (B) TYPE: nucleic acid
81              (C) STRANDEDNESS: unknown
82              (D) TOPOLOGY: linear
83      (ii) MOLECULE TYPE: cDNA
84     (iii) HYPOTHETICAL: NO
85      (iv) ANTI-SENSE: NO
86       (v) FRAGMENT TYPE: internal
87      (vi) ORIGINAL SOURCE:
88              (A) ORGANISM: Homo sapiens
89      (ix) FEATURE:
90              (A) NAME/KEY: CDS
91              (B) LOCATION: 283..1791
92      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
94 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA    60
96 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC   120
98 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT   180
100 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA   240
102 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC     294
103                                               Met Thr Leu Gly
104                                                1
106 TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG    342
107 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
108   5                  10                  15                  20
110 GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT    390
111 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
112              25                  30                  35
114 GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA    438
115 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
116              40                  45                  50
118 GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC    486
119 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
120              55                  60                  65
122 TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC    534
123 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
124      70                  75                  80
126 GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC    582
127 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
128 85                  90                  95                 100
130 CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT    630
131 Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp
132             105                 110                 115
134 GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG    678
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135 Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu
136           120               125               130
138 GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG      726
139 Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu
140           135               140               145
142 AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG      774
143 Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu
144     150               155               160
146 AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT      822
147 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser
148 165               170               175               180
150 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG      870
151 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg
152               185               190               195
154 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC      918
155 Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg
156           200               205               210
158 TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC      966
159 Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val
160           215               220               225
162 AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG     1014
163 Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu
164     230               235               240
166 ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC     1062
167 Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile
168 245               250               255               260
170 GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC     1110
171 Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile
172               265               270               275
174 ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG     1158
175 Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln
176           280               285               290
178 ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC     1206
179 Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys
180           295               300               305
182 GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA     1254
183 Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro
184     310               315               320
186 GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC     1302
187 Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser
188 325               330               335               340
190 AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA     1350
191 Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser
192               345               350               355
194 CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC     1398
195 Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr
196           360               365               370
198 AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC     1446
199 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
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200        375                    380                  385
202 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG        1494
203 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
204     390                    395                  400
206 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC        1542
207 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
208 405                    410                  415                  420
210 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG        1590
211 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
212                    425                  430                  435
214 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT        1638
215 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
216            440                  445                  450
218 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG        1686
219 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
220            455                  460                  465
222 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG        1734
223 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
224     470                    475                  480
226 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA        1782
227 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
228 485                    490                  495                  500
230 GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC              1831
231 Val Ile Gln
233 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG     1891
235 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT     1951
237 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA                                  1984
241 (2) INFORMATION FOR SEQ ID NO: 2:
242       (i) SEQUENCE CHARACTERISTICS:
243            (A) LENGTH: 503 amino acids
244            (B) TYPE: amino acid
245            (D) TOPOLOGY: linear
246       (ii) MOLECULE TYPE: protein
247       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
249 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
250   1             5                   10                  15
252 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
253            20                   25                  30
255 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
256        35                   40                  45
258 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
259     50                   55                  60
261 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
262 65                   70                  75                  80
264 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
265                85                   90                  95
267 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
268            100                  105                  110
270 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
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271          115                    120                    125
273 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
274      130                    135                    140
276 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
277 145                    150                    155                    160
279 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
280              165                    170                    175
282 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
283              180                    185                    190
285 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
286          195                    200                    205
288 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
289      210                    215                    220
291 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
292 225                    230                    235                    240
294 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
295              245                    250                    255
297 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
298              260                    265                    270
300 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
301          275                    280                    285
303 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
304          290                    295                    300
306 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
307 305                    310                    315                    320
309 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
310              325                    330                    335
312 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
313              340                    345                    350
315 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
316          355                    360                    365
318 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
319      370                    375                    380
321 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
322 385                    390                    395                    400
324 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
325              405                    410                    415
327 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
328          420                    425                    430
330 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
331          435                    440                    445
333 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
334      450                    455                    460
336 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
337 465                    470                    475                    480
339 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
340              485                    490                    495
342 Glu Lys Pro Lys Val Ile Gln
343          500
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VERIFICATION SUMMARY   DATE: 01/16/2002
PATENT APPLICATION: US/09/903,068   TIME: 15:53:54

Input Set : N:\Crf3\RULE60\09903068.raw
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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:2726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26